AMENDMENTS TO THE CLAIMS

Listing of Claims

1. (Previously presented) A method for the fermentative production of L-methionine, which comprises the following steps:

   a) fermenting in a medium cells of coryneform bacterium *Corynebacterium glutamicum* for producing L-methionine, said coryneform bacteria expressing at least one heterologous nucleotide sequence which codes for a protein with homoserine O-acetyltransferase (metA) activity, wherein said heterologous nucleotide sequence comprises a nucleotide sequence encoding a metA protein derived from *Corynebacterium diphteriae* having an amino acid sequence as set forth in SEQ ID NO: 2;

   b) concentrating L-methionine in the medium or in the bacterial cells, and

   c) isolating L-methionine.

2-4. (Cancelled)

5. (Previously presented) The method as claimed in claim 1, wherein the metA-encoding nucleotide sequence comprises a coding sequence as set forth in SEQ ID NO:1.

6. (Cancelled)

7. (Previously presented) The method as claimed in claim 1, wherein the coding metA sequence is a DNA or RNA which can be replicated in coryneform bacteria or is stably integrated into the chromosome.

8. (Previously presented) The method as claimed in claim 7, wherein

   a) a bacteria strain transformed with a plasmid vector carrying at least one copy of the coding metA sequence under the control of regulatory sequences is used, or

   b) a strain in which the coding metA sequence has been integrated into the bacteria chromosome is used.

9. (Previously presented) The method as claimed in claim 1, wherein the coding metA sequence is overexpressed.

10. (Currently amended) The method as claimed in claim 1, wherein bacteria are fermented in which additionally at least one further gene of the biosynthetic pathway of L-methionine has been ~~amplified or mutated~~ overexpressed such that its activity is not influenced by metabolic metabolites.

11. (Cancelled)

12. (Currently amended) The method of claim 1, wherein coryneform bacteria are fermented in which, at the same time, a lysC gene derived from a coryneform bacterium, which encodes an aspartate kinase, is overexpressed ~~or mutated in such a way that the activity of the corresponding protein is influenced by metabolic metabolites to a smaller extent, if at all, compared to a nonmutated protein~~.

13. (Cancelled)

14. (Previously presented) The method of claim 17, wherein the coryneform bacterium is of the species *Corynebacterium glutamicum*.

15-16. (Cancelled)

17. (Currently amended) A method for the production of L-methionine, which comprises the following steps:

a) fermenting in a medium cells of a coryneform bacterium for producing L-methionine, said coryneform bacteria expressing at least one heterologous nucleotide sequence which codes for a protein with homoserine O-acetyltransferase (metA) activity, wherein the heterologous ~~metA-encoding~~ nucleotide sequence ~~is less than 100% homologous to the metA-encoding~~

~~sequence from *Corynebacterium glutamicum* ATCC 13032~~ comprises a nucleotide sequence having 95% identity or more to the sequence as set forth in SEQ ID NO: 1;

b) concentrating L-methionine in the medium or in the bacterial cells; and

c) isolating L-methionine.

18. (Previously presented) The method of claim 17, wherein the metA-encoding nucleotide sequence comprises a coding sequence as set forth in SEQ ID NO:1.

19. (Currently amended) The method of claim 17, wherein the metA-encoding nucleotide sequence codes for a protein with metA activity, said protein comprising an amino acid sequence as set forth in SEQ ID NO: 2 ~~or a fragment of SEQ ID NO: 2 having metA activity~~.

20. (Previously presented) The method of claim 17, wherein the coding metA sequence is a DNA or RNA which can be replicated in coryneform bacteria or is stably integrated into the chromosome.

21. (Previously presented) The method of claim 17, wherein

a) a bacteria strain transformed with a plasmid vector carrying at least one copy of the coding metA sequence under the control of regulatory sequences is used, or

b) a strain in which the coding metA sequence has been integrated into the bacteria chromosome is used.

22. (Previously presented) The method of claim 17, wherein the coding metA sequence is overexpressed.

23. (Currently amended) The method of claim 17, wherein bacteria are fermented in which additionally at least one further gene of the biosynthetic pathway of L-methionine has been ~~amplified or mutated~~ overexpressed such that its activity is not influenced by metabolic metabolites.

24. (Currently amended) A method for the production of L-methionine, which comprises the following steps:

a) fermenting in a medium cells of a coryneform bacterium for producing of L-methionine, said coryneform bacteria expressing at least one heterologous nucleotide sequence which codes for a protein with homoserine O-acetyltransferase (metA) activity, wherein said heterologous nucleotide sequence comprises a nucleotide sequence encoding a metA protein having an amino acid sequence with 95% homology or more to the sequence as set forth in SEQ ID NO: 2 derived from *Corynebacterium diphteriae*;

b) concentrating L-methionine in the medium or in the bacterial cells; and

c) isolating L-methionine.

25-26. (Cancelled)

27. (Previously presented) The method of claim 24, wherein the coding metA sequence is a DNA or RNA which can be replicated in coryneform bacteria or is stably integrated into the chromosome.

28. (Previously presented) The method of claim 24, wherein

a) a bacteria strain transformed with a plasmid vector carrying at least one copy of the coding metA sequence under the control of regulatory sequences is used, or

b) a strain in which the coding metA sequence has been integrated into the bacteria chromosome is used.

29. (Previously presented) The method of claim 24, wherein the coding metA sequence is overexpressed.

30. (Currently amended) The method of claim 24, wherein bacteria are fermented in which additionally at least one further gene of the biosynthetic pathway of L-methionine has been ~~amplified or mutated~~ overexpressed such that its activity is not influenced by metabolic metabolites.

31. (Previously presented) The method of claim 24, wherein the coryneform bacterium is of the species *Corynebacterium glutamicum*.